

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/509,484
Source: P4/10
Date Processed by STIC: 11/2/05

ENTERED



PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/509,484

DATE: 11/02/2005

TIME: 09:41:02

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\11022005\J509484.raw

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3 <110> APPLICANT: Takeda Chemical Industries, Ltd.
5 <120> TITLE OF INVENTION: Novel Screening Method
7 <130> FILE REFERENCE: P04-117PCT
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/509,484
C--> 9 <141> CURRENT FILING DATE: 2004-09-27
9 <150> PRIOR APPLICATION NUMBER: JP 2002-093045
10 <151> PRIOR FILING DATE: 2002-03-28
12 <150> PRIOR APPLICATION NUMBER: JP 2002-361580
13 <151> PRIOR FILING DATE: 2002-12-13
15 <160> NUMBER OF SEQ ID NOS: 10
17 <170> SOFTWARE: PatentIn version 3.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 957
21 <212> TYPE: DNA
22 <213> ORGANISM: Rattus sp.
24 <220> FEATURE:
25 <221> NAME/KEY: CDS
26 <222> LOCATION: (1)..(957)
27 <223> OTHER INFORMATION: rat-derived rCB7T084
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33 ccc acc atg gac cct gtg acc tgg gtt tac ttt tca gtg aca ttc ctg      96
34 Pro Thr Met Asp Pro Val Thr Trp Val Tyr Phe Ser Val Thr Phe Leu
35          20          25          30
36 gcc atg gcc acc tgt gtg tgt ggg ata gtg ggc aac tcc atg gtg att      144
37 Ala Met Ala Thr Cys Val Cys Gly Ile Val Gly Asn Ser Met Val Ile
38          35          40          45
39 tgg cta ctg agt ttc cac agt gtg cag agg tcc ccc ttc tgc acc tac      192
40 Trp Leu Leu Ser Phe His Ser Val Gln Arg Ser Pro Phe Cys Thr Tyr
41          50          55          60
42 gtg ctc aac ctg gcg gtg gcc gac ctc ctc ttc ctg ctc tgc atg gcc      240
43 Val Leu Asn Leu Ala Val Ala Asp Leu Leu Phe Leu Leu Cys Met Ala
44 65          70          75          80
45 tcc ctg ctc agt ctg gaa aca ggg ccc ctg ctc aca gcc agc acc tcc      288
46 Ser Leu Leu Ser Leu Glu Thr Gly Pro Leu Leu Thr Ala Ser Thr Ser
47          85          90          95
48 gcc aga gtc tac gag ggg atg aag aga atc aag tac ttt gcc tac aca      336
49 Ala Arg Val Tyr Glu Gly Met Lys Arg Ile Lys Tyr Phe Ala Tyr Thr
50          100         105         110
51 gca ggc ctg agc ctg ctg acg gcc atc agc acc cag cgc tgt ctc tcc      384
52 Ala Gly Leu Ser Leu Leu Thr Ala Ile Ser Thr Gln Arg Cys Leu Ser

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54 gtg ctt ttc ccc atc tgg tat aag tgc cac cgg ccc cag cac ctg tcg      432
55 Val Leu Phe Pro Ile Trp Tyr Lys Cys His Arg Pro Gln His Leu Ser
56          130          135          140
57 ggg gtg gta tgt ggt gtg ctg tgg gca ctg gcc ctc ctg atg aac ttc      480
58 Gly Val Val Cys Gly Val Leu Trp Ala Leu Ala Leu Leu Met Asn Phe
59 145          150          155          160
60 ctg gct tct ttc ttc tgt gtt caa ttc tgg cat ccc gac aaa tac cag      528
61 Leu Ala Ser Phe Phe Cys Val Gln Phe Trp His Pro Asp Lys Tyr Gln
62          165          170          175
63 tgc ttc aag gtg gac atg gtt ttc aac agt ctt atc ctg ggg atc ttc      576
64 Cys Phe Lys Val Asp Met Val Phe Asn Ser Leu Ile Leu Gly Ile Phe
65          180          185          190
66 atg ccc gtc atg gtc ctg acc agc gcc atc atc ttc atc cgc atg cga      624
67 Met Pro Val Met Val Leu Thr Ser Ala Ile Ile Phe Ile Arg Met Arg
68          195          200          205
69 aag aac agc ctg ctg cag aga cgg cag cct cgg cgg ctc tac gtg gtc      672
70 Lys Asn Ser Leu Leu Gln Arg Arg Gln Pro Arg Arg Leu Tyr Val Val
71          210          215          220
72 atc ctg act tcc gtc ctt gtc ttc ctt acc tgt tct ctg ccg ttg ggc      720
73 Ile Leu Thr Ser Val Leu Val Phe Leu Thr Cys Ser Leu Pro Leu Gly
74 225          230          235          240
75 atc aac tgg ttc tta ctc tac tgg gtg gaa ctg ccg cag gcc gtg agg      768
76 Ile Asn Trp Phe Leu Leu Tyr Trp Val Glu Leu Pro Gln Ala Val Arg
77          245          250          255
78 ctc ctg tac gtc tgc tca tca cgc ttc tcc tcg tct ttg agc agc agc      816
79 Leu Leu Tyr Val Cys Ser Ser Arg Phe Ser Ser Ser Leu Ser Ser Ser
80          260          265          270
81 gcc aac cca gtc atc tac ttc ctc gtg ggc agc cag aag agc cac cgg      864
82 Ala Asn Pro Val Ile Tyr Phe Leu Val Gly Ser Gln Lys Ser His Arg
83          275          280          285
84 ctg cag gag tct ctg ggt gct gtg ctg ggg cgg gca ctt cag gac gag      912
85 Leu Gln Glu Ser Leu Gly Ala Val Leu Gly Arg Ala Leu Gln Asp Glu
86          290          295          300
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92 <211> LENGTH: 319
93 <212> TYPE: PRT
94 <213> ORGANISM: Rattus sp.
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99 Pro Thr Met Asp Pro Val Thr Trp Val Tyr Phe Ser Val Thr Phe Leu
100          20          25          30
101 Ala Met Ala Thr Cys Val Cys Gly Ile Val Gly Asn Ser Met Val Ile
102          35          40          45
103 Trp Leu Leu Ser Phe His Ser Val Gln Arg Ser Pro Phe Cys Thr Tyr

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105 Val Leu Asn Leu Ala Val Ala Asp Leu Leu Phe Leu Leu Cys Met Ala
106 65      70      75      80
107 Ser Leu Leu Ser Leu Glu Thr Gly Pro Leu Leu Thr Ala Ser Thr Ser
108      85      90      95
109 Ala Arg Val Tyr Glu Gly Met Lys Arg Ile Lys Tyr Phe Ala Tyr Thr
110      100      105      110
111 Ala Gly Leu Ser Leu Leu Thr Ala Ile Ser Thr Gln Arg Cys Leu Ser
112      115      120      125
113 Val Leu Phe Pro Ile Trp Tyr Lys Cys His Arg Pro Gln His Leu Ser
114      130      135      140
115 Gly Val Val Cys Gly Val Leu Trp Ala Leu Ala Leu Leu Met Asn Phe
116 145      150      155      160
117 Leu Ala Ser Phe Phe Cys Val Gln Phe Trp His Pro Asp Lys Tyr Gln
118      165      170      175
119 Cys Phe Lys Val Asp Met Val Phe Asn Ser Leu Ile Leu Gly Ile Phe
120      180      185      190
121 Met Pro Val Met Val Leu Thr Ser Ala Ile Ile Phe Ile Arg Met Arg
122      195      200      205
123 Lys Asn Ser Leu Leu Gln Arg Arg Gln Pro Arg Arg Leu Tyr Val Val
124      210      215      220
125 Ile Leu Thr Ser Val Leu Val Phe Leu Thr Cys Ser Leu Pro Leu Gly
126 225      230      235      240
127 Ile Asn Trp Phe Leu Leu Tyr Trp Val Glu Leu Pro Gln Ala Val Arg
128      245      250      255
129 Leu Leu Tyr Val Cys Ser Ser Arg Phe Ser Ser Ser Leu Ser Ser Ser
130      260      265      270
131 Ala Asn Pro Val Ile Tyr Phe Leu Val Gly Ser Gln Lys Ser His Arg
132      275      280      285
133 Leu Gln Glu Ser Leu Gly Ala Val Leu Gly Arg Ala Leu Gln Asp Glu
134      290      295      300
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138 <210> SEQ ID NO: 3
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140 <212> TYPE: DNA
141 <213> ORGANISM: Homo sapiens
143 <220> FEATURE:
144 <221> NAME/KEY: CDS
145 <222> LOCATION: (1)..(963)
146 <223> OTHER INFORMATION: human-derived TGR7
148 <400> SEQUENCE: 3
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151 1      5      10      15
152 tat tcc aga ggg agc aca gtg cac acg gcc tac ctg gtg ctg agc tcc      96
153 Tyr Ser Arg Gly Ser Thr Val His Thr Ala Tyr Leu Val Leu Ser Ser
154      20      25      30
155 ctg gcc atg ttc acc tgc ctg tgc ggg atg gca ggc aac agc atg gtg      144

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156	Leu	Ala	Met	Phe	Thr	Cys	Leu	Cys	Gly	Met	Ala	Gly	Asn	Ser	Met	Val	
157			35					40					45				
158	atc	tgg	ctg	ctg	ggc	ttt	cga	atg	cac	agg	aac	ccc	ttc	tgc	atc	tat	192
159	Ile	Trp	Leu	Leu	Gly	Phe	Arg	Met	His	Arg	Asn	Pro	Phe	Cys	Ile	Tyr	
160		50					55					60					
161	atc	ctc	aac	ctg	gcg	gca	gcc	gac	ctc	ctc	ttc	ctc	ttc	agc	atg	gct	240
162	Ile	Leu	Asn	Leu	Ala	Ala	Asp	Leu	Leu	Phe	Leu	Phe	Ser	Met	Ala		
163	65				70					75						80	
164	tcc	acg	ctc	agc	ctg	gaa	acc	cag	ccc	ctg	gtc	aat	acc	act	gac	aag	288
165	Ser	Thr	Leu	Ser	Leu	Glu	Thr	Gln	Pro	Leu	Val	Asn	Thr	Thr	Asp	Lys	
166					85				90						95		
167	gtc	cac	gag	ctg	atg	aag	aga	ctg	atg	tac	ttt	gcc	tac	aca	gtg	ggc	336
168	Val	His	Glu	Leu	Met	Lys	Arg	Leu	Met	Tyr	Phe	Ala	Tyr	Thr	Val	Gly	
169					100				105					110			
170	ctg	agc	ctg	ctg	acg	gcc	atc	agc	acc	cag	cgc	tgt	ctc	tct	gtc	ctc	384
171	Leu	Ser	Leu	Leu	Thr	Ala	Ile	Ser	Thr	Gln	Arg	Cys	Leu	Ser	Val	Leu	
172			115					120					125				
173	ttc	cct	atc	tgg	ttc	aag	tgt	cac	cgg	ccc	agg	cac	ctg	tca	gcc	tgg	432
174	Phe	Pro	Ile	Trp	Phe	Lys	Cys	His	Arg	Pro	Arg	His	Leu	Ser	Ala	Trp	
175		130				135					140						
176	gtg	tgt	ggc	ctg	ctg	tgg	acg	ctc	tgt	ctc	ctg	atg	aac	ggg	ttg	acc	480
177	Val	Cys	Gly	Leu	Leu	Trp	Thr	Leu	Cys	Leu	Met	Asn	Gly	Leu	Thr		
178	145					150				155					160		
179	tct	tcc	ttc	tgc	agc	aag	ttc	ttg	aaa	ttc	aat	gaa	gat	cgg	tgc	ttc	528
180	Ser	Ser	Phe	Cys	Ser	Lys	Phe	Leu	Lys	Phe	Asn	Glu	Asp	Arg	Cys	Phe	
181					165				170					175			
182	agg	gtg	gac	atg	gtc	cag	gcc	gcc	ctc	atc	atg	ggg	gtc	tta	acc	cca	576
183	Arg	Val	Asp	Met	Val	Gln	Ala	Ala	Leu	Ile	Met	Gly	Val	Leu	Thr	Pro	
184					180				185					190			
185	gtg	atg	act	ctg	tcc	agc	ctg	acc	ctc	ttt	gtc	tgg	gtg	cgg	agg	agc	624
186	Val	Met	Thr	Leu	Ser	Ser	Leu	Thr	Leu	Phe	Val	Trp	Val	Arg	Arg	Ser	
187					195			200					205				
188	tcc	cag	cag	tgg	cgg	cgg	cag	ccc	aca	cgg	ctg	ttc	gtg	gtg	gtc	ctg	672
189	Ser	Gln	Gln	Trp	Arg	Arg	Gln	Pro	Thr	Arg	Leu	Phe	Val	Val	Val	Leu	
190		210				215					220						
191	gcc	tct	gtc	ctg	gtg	ttc	ctc	atc	tgt	tcc	ctg	cct	ctg	agc	atc	tac	720
192	Ala	Ser	Val	Leu	Val	Phe	Leu	Ile	Cys	Ser	Leu	Pro	Leu	Ser	Ile	Tyr	
193	225					230					235				240		
194	tgg	ttt	gtg	ctc	tac	tgg	ttg	agc	ctg	ccg	ccc	gag	atg	cag	gtc	ctg	768
195	Trp	Phe	Val	Leu	Tyr	Trp	Leu	Ser	Leu	Pro	Pro	Glu	Met	Gln	Val	Leu	
196					245				250					255			
197	tgc	ttc	agc	ttg	tca	cgc	ctc	tcc	tcg	tcc	gta	agc	agc	agc	gcc	aac	816
198	Cys	Phe	Ser	Leu	Ser	Arg	Leu	Ser	Ser	Ser	Val	Ser	Ser	Ser	Ala	Asn	
199					260			265						270			
200	ccc	gtc	atc	tac	ttc	ctg	gtg	ggc	agc	cgg	agg	agc	cac	agg	ctg	ccc	864
201	Pro	Val	Ile	Tyr	Phe	Leu	Val	Gly	Ser	Arg	Arg	Ser	His	Arg	Leu	Pro	
202					275			280					285				
203	acc	agg	tcc	ctg	ggg	act	gtg	ctc	caa	cag	gcg	ctt	cgc	gag	gag	ccc	912
204	Thr	Arg	Ser	Leu	Gly	Thr	Val	Leu	Gln	Gln	Ala	Leu	Arg	Glu	Glu	Pro	

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205      290      295      300
206 gag ctg gaa ggt ggg gag acg ccc acc gtg ggc acc aat gag atg ggg      960
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208 305      310      315      320
209 gct
210 Ala
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213 <211> LENGTH: 321
214 <212> TYPE: PRT
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217 <400> SEQUENCE: 4
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221      20      25      30
222 Leu Ala Met Phe Thr Cys Leu Cys Gly Met Ala Gly Asn Ser Met Val
223      35      40      45
224 Ile Trp Leu Leu Gly Phe Arg Met His Arg Asn Pro Phe Cys Ile Tyr
225      50      55      60
226 Ile Leu Asn Leu Ala Ala Asp Leu Leu Phe Leu Phe Ser Met Ala
227 65      70      75      80
228 Ser Thr Leu Ser Leu Glu Thr Gln Pro Leu Val Asn Thr Thr Asp Lys
229      85      90      95
230 Val His Glu Leu Met Lys Arg Leu Met Tyr Phe Ala Tyr Thr Val Gly
231      100      105      110
232 Leu Ser Leu Leu Thr Ala Ile Ser Thr Gln Arg Cys Leu Ser Val Leu
233      115      120      125
234 Phe Pro Ile Trp Phe Lys Cys His Arg Pro Arg His Leu Ser Ala Trp
235      130      135      140
236 Val Cys Gly Leu Leu Trp Thr Leu Cys Leu Leu Met Asn Gly Leu Thr
237 145      150      155      160
238 Ser Ser Phe Cys Ser Lys Phe Leu Lys Phe Asn Glu Asp Arg Cys Phe
239      165      170      175
240 Arg Val Asp Met Val Gln Ala Ala Leu Ile Met Gly Val Leu Thr Pro
241      180      185      190
242 Val Met Thr Leu Ser Ser Leu Thr Leu Phe Val Trp Val Arg Arg Ser
243      195      200      205
244 Ser Gln Gln Trp Arg Arg Gln Pro Thr Arg Leu Phe Val Val Val Leu
245      210      215      220
246 Ala Ser Val Leu Val Phe Leu Ile Cys Ser Leu Pro Leu Ser Ile Tyr
247 225      230      235      240
248 Trp Phe Val Leu Tyr Trp Leu Ser Leu Pro Pro Glu Met Gln Val Leu
249      245      250      255
250 Cys Phe Ser Leu Ser Arg Leu Ser Ser Ser Val Ser Ser Ser Ala Asn
251      260      265      270
252 Pro Val Ile Tyr Phe Leu Val Gly Ser Arg Arg Ser His Arg Leu Pro
253      275      280      285
254 Thr Arg Ser Leu Gly Thr Val Leu Gln Gln Ala Leu Arg Glu Glu Pro
255      290      295      300

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VERIFICATION SUMMARY

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DATE: 11/02/2005

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Input Set : A:\PTO.RJ.txt

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date